



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2025 – 02:17 PM JST

PDB ID : 8HKM / pdb_00008hkm
EMDB ID : EMD-34855
Title : ion channel
Authors : Jiang, D.H.; Zhang, J.T.
Deposited on : 2022-11-27
Resolution : 2.95 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

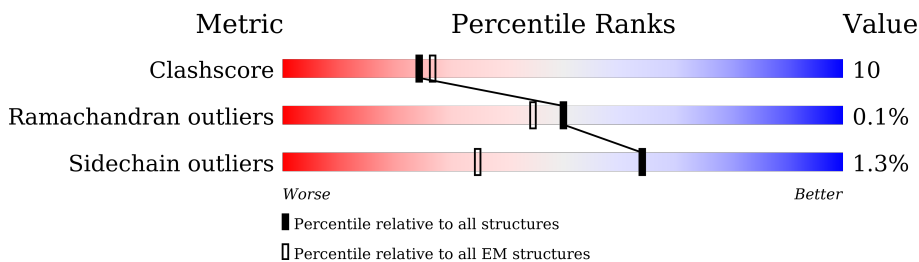
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.95 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1235	<div> <div>11%</div> <div>55%</div> <div>17%</div> <div>27%</div> </div>
1	B	1235	<div> <div>11%</div> <div>58%</div> <div>14%</div> <div>27%</div> </div>
1	C	1235	<div> <div>12%</div> <div>56%</div> <div>17%</div> <div>27%</div> </div>
1	D	1235	<div> <div>11%</div> <div>57%</div> <div>16%</div> <div>27%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 28855 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Potassium channel subfamily T member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	899	Total	C	N	O	S	0	0
			7188	4658	1196	1281	53		
1	B	899	Total	C	N	O	S	0	0
			7188	4658	1196	1281	53		
1	C	899	Total	C	N	O	S	0	0
			7188	4658	1196	1281	53		
1	D	899	Total	C	N	O	S	0	0
			7188	4658	1196	1281	53		

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

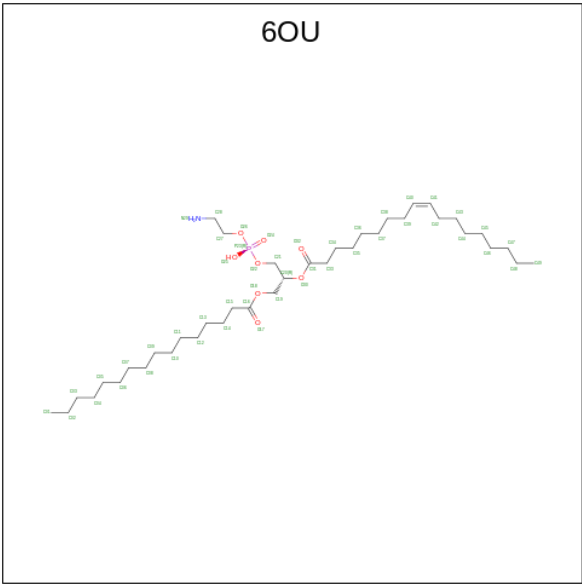
Mol	Chain	Residues	Atoms		AltConf
2	A	4	Total	K	0
			4	4	
2	B	2	Total	K	0
			2	2	
2	C	2	Total	K	0
			2	2	
2	D	3	Total	K	0
			3	3	

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	

- Molecule 4 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-p

ropan-2-yl] ({Z})-octadec-9-enoate (CCD ID: 6OU) (formula: C₃₉H₇₆NO₈P) (labeled as "Ligand of Interest" by depositor).

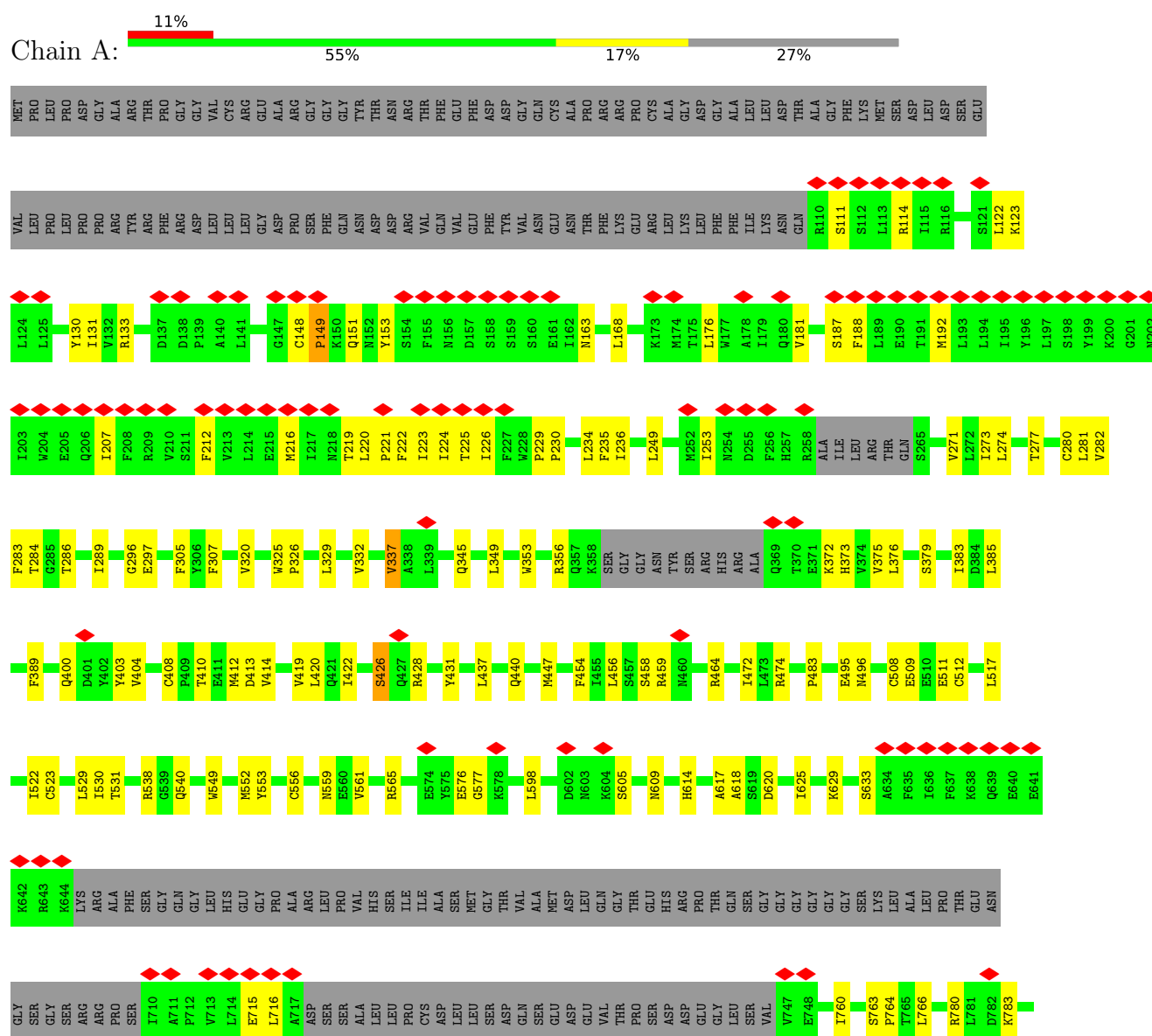


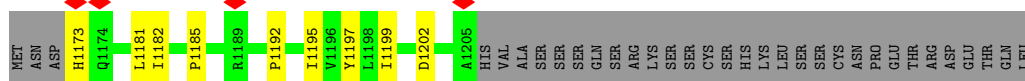
Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	O	P	0
			22	15	6	1	
4	B	1	Total	C	O	P	0
			22	15	6	1	
4	C	1	Total	C	O	P	0
			22	15	6	1	
4	D	1	Total	C	O	P	0
			22	15	6	1	

3 Residue-property plots

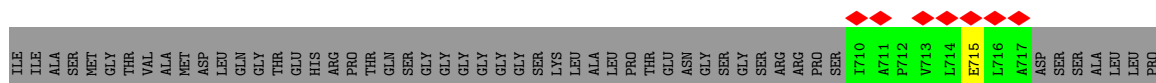
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Potassium channel subfamily T member 1

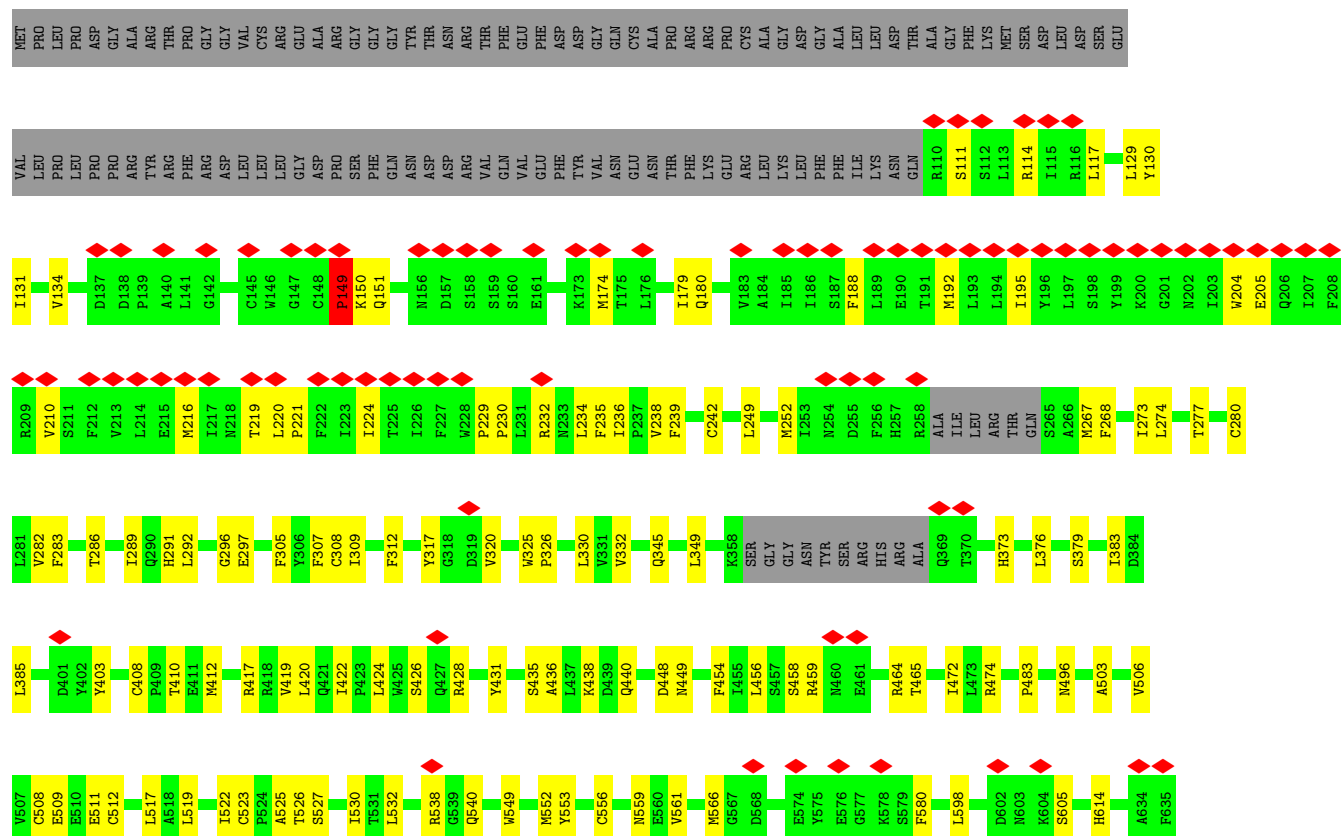




- Molecule 1: Potassium channel subfamily T member 1



- Molecule 1: Potassium channel subfamily T member 1





N559	E560	V561	I564	D568	E574	Y575	E576	G577	K578	L598	K599	R600	E601	D602	N603	K604	S605	H614	A617	D620	I625	T628	K629	E630	S633	A634	F635	I636	F637	K638	Q639	E640	E641	K642	R643	K644	LYS	ARG	ALA	PHE	SER	GLY	GLN	GLY	LEU	HIS	GLU	PRO	
ASP	SER	SER	ALA	LEU	CYS	ASP	LEU	SER	ASP	GLN	SER	GLU	ASP	VAL	THR	THR	GLY	ASP	GLU	HIS	ARG	PRO	THR	SER	GLY	LYS	ALA	PRO	THR	THR	GLU	ASN	SER	SER	ARG	ARG	PRO	SER	I710	A711	P712	V713	L714	E715	L716	A717			
R822	A823	Y824	R828	K829	H844	H845	E848	M855	M859	E860	G861	S862	Y863	D864	D867	Q871	C872	V881	D884	K885	E886	SER	THR	MET	L765	L766	R780	D782	K783	G784	C785	K786	H787	N788	S789	Y790	E791	K794	F798	L802	I803	I804	L821						
L940	S943	K944	K947	R948	E949	R950	E951	G967	I972	S973	M974	L975	D976	S982	K985	R993	T1001	P1002	C1008	A1009	I1012	T1013	E1014	G1015	D1016	L1017	R1020	L1029	A1034	I1038	Y1041	R1042	V1047	F1048	SER	THR	SER	GLU	PRO	HIS	ASP	LEU							
ARG	ALA	GLN	SER	ILE	SER	VAL	ASN	VAL	GLU	ASP	CYS	GLU	ASP	THR	ARG	GLU	VAL	LYS	PRO	GLY	TRP	GLY	SER	ARG	ALA	GLY	THR	GLY	SER	GLN	GLY	ASP	PRO	ALA	GLU	HIS	PRO	LEU	ARG	ARG	LYS	SER	LEU	GLN	TRP	ALA	ARG	ARG	LEU
SER	ARG	LYS	ALA	PRO	LYS	GLN	ALA	ARG	ALA	A1128	A1129	A1130	E1131	W1132	I1133	S1134	Q1135	Q1136	R1137	R1142	R1143	R1146	L1149	V1153	R1156	M1157	K1158	H1159	P1163	T1164	T1165	D1168	GLU	MET	ASN	ASP	H1173	Q1174	V1180	L1181	P1184	P1185	T1188	R1189	P1192	I1195			
V1196	Y1197	L1198	I1199	D1202	A1205	HIS	VAL	ALA	SER	SER	SER	GLN	SER	ARG	LYS	SER	CYS	SER	HIS	LYS	LEU	SER	CYS	ASN	PRO	GLU	THR	ARG	GLU	THR	GLN	LEU																	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24190	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.947	Depositor
Minimum map value	-0.627	Depositor
Average map value	0.033	Depositor
Map value standard deviation	0.123	Depositor
Recommended contour level	0.612	Depositor
Map size (\AA)	266.24, 266.24, 266.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 6OU, K, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.14	0/7356	0.34	0/9981
1	B	0.12	0/7356	0.32	1/9981 (0.0%)
1	C	0.12	0/7356	0.33	1/9981 (0.0%)
1	D	0.13	0/7356	0.46	8/9981 (0.1%)
All	All	0.13	0/29424	0.36	10/39924 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	149	PRO	CB-CA-C	17.92	141.12	111.56
1	D	150	LYS	N-CA-C	-16.07	76.57	110.80
1	D	150	LYS	N-CA-CB	10.89	128.90	110.49
1	C	149	PRO	N-CA-C	7.33	127.57	112.47
1	B	149	PRO	N-CA-C	7.32	127.56	112.47

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	149	PRO	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7188	0	7185	174	0
1	B	7188	0	7187	140	0
1	C	7188	0	7185	166	0
1	D	7188	0	7186	151	0
2	A	4	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	22	0	0	0	0
4	B	22	0	0	0	0
4	C	22	0	0	0	0
4	D	22	0	0	0	0
All	All	28855	0	28743	603	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 603 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:828:ARG:CZ	1:D:829:LYS:HZ1	0.94	1.57
1:C:538:ARG:HH12	1:C:540:GLN:NE2	1.03	1.52
1:D:828:ARG:CZ	1:D:829:LYS:NZ	1.79	1.43
1:B:538:ARG:HH12	1:B:540:GLN:NE2	1.18	1.36
1:C:532:LEU:CD2	1:C:959:MET:HE2	1.56	1.34

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	883/1235 (72%)	856 (97%)	26 (3%)	1 (0%)	48	72
1	B	883/1235 (72%)	858 (97%)	24 (3%)	1 (0%)	48	72
1	C	883/1235 (72%)	861 (98%)	21 (2%)	1 (0%)	48	72
1	D	883/1235 (72%)	860 (97%)	22 (2%)	1 (0%)	48	72
All	All	3532/4940 (72%)	3435 (97%)	93 (3%)	4 (0%)	50	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	PRO
1	B	149	PRO
1	C	149	PRO
1	D	149	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	790/1086 (73%)	778 (98%)	12 (2%)	60	78
1	B	790/1086 (73%)	779 (99%)	11 (1%)	62	79
1	C	790/1086 (73%)	782 (99%)	8 (1%)	73	85
1	D	790/1086 (73%)	780 (99%)	10 (1%)	65	80
All	All	3160/4344 (73%)	3119 (99%)	41 (1%)	64	80

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	876	TYR
1	D	471	THR
1	C	984	VAL
1	D	192	MET
1	D	529	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	449	ASN
1	C	844	HIS
1	D	845	HIS
1	C	470	GLN
1	C	543	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 15 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	6OU	B	1301	-	21,21,48	1.13	3 (14%)	23,24,53	1.28	2 (8%)
4	6OU	C	1301	-	21,21,48	1.13	3 (14%)	23,24,53	1.29	2 (8%)
4	6OU	A	1304	-	21,21,48	1.12	3 (14%)	23,24,53	1.34	2 (8%)
4	6OU	D	1301	-	21,21,48	1.13	3 (14%)	23,24,53	1.33	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	6OU	B	1301	-	-	10/21/21/52	-
4	6OU	C	1301	-	-	10/21/21/52	-
4	6OU	A	1304	-	-	7/21/21/52	-
4	6OU	D	1301	-	-	10/21/21/52	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1301	6OU	O30-C31	-3.42	1.33	1.43
4	C	1301	6OU	O30-C31	-3.40	1.33	1.43
4	A	1304	6OU	O30-C31	-3.38	1.33	1.43
4	B	1301	6OU	O30-C31	-3.37	1.33	1.43
4	B	1301	6OU	P23-O26	2.44	1.64	1.54

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1304	6OU	O26-P23-O22	-4.82	93.90	106.73
4	D	1301	6OU	O26-P23-O22	-4.80	93.97	106.73
4	C	1301	6OU	O26-P23-O22	-4.76	94.08	106.73
4	B	1301	6OU	O26-P23-O22	-4.73	94.15	106.73
4	C	1301	6OU	O25-P23-O24	2.08	118.83	110.68

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1301	6OU	C21-O22-P23-O24
4	B	1301	6OU	C21-O22-P23-O25

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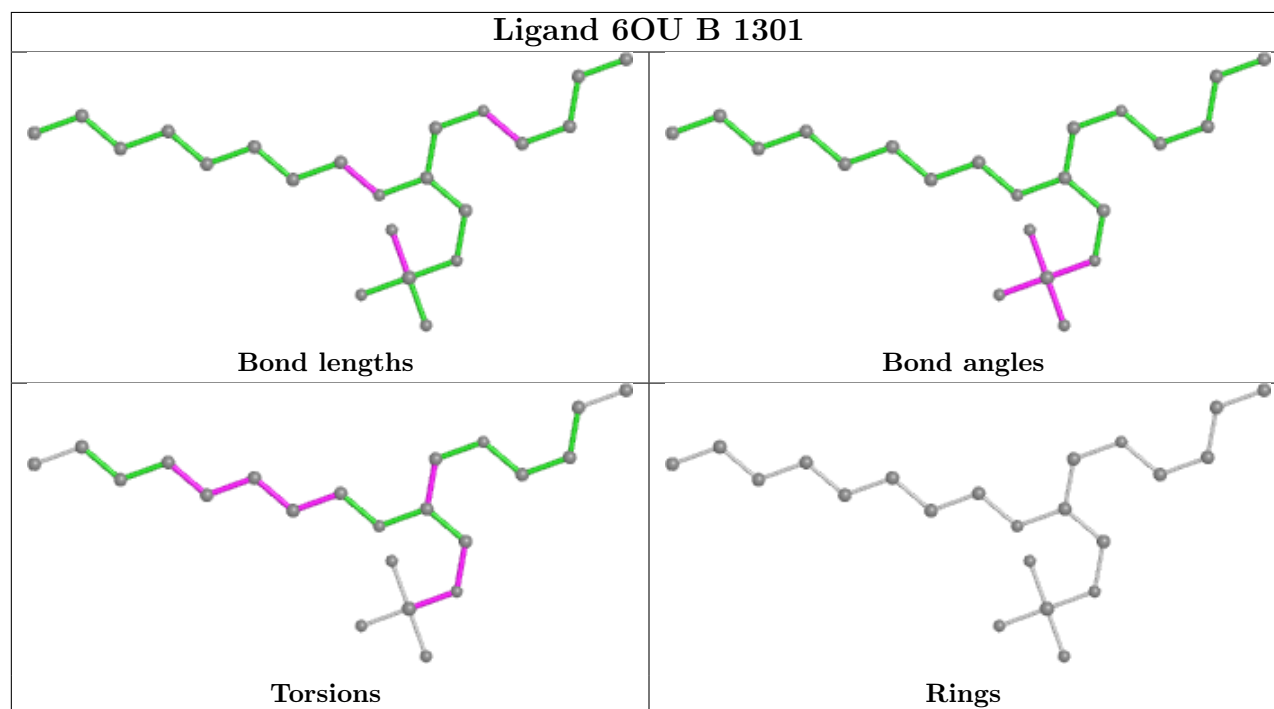
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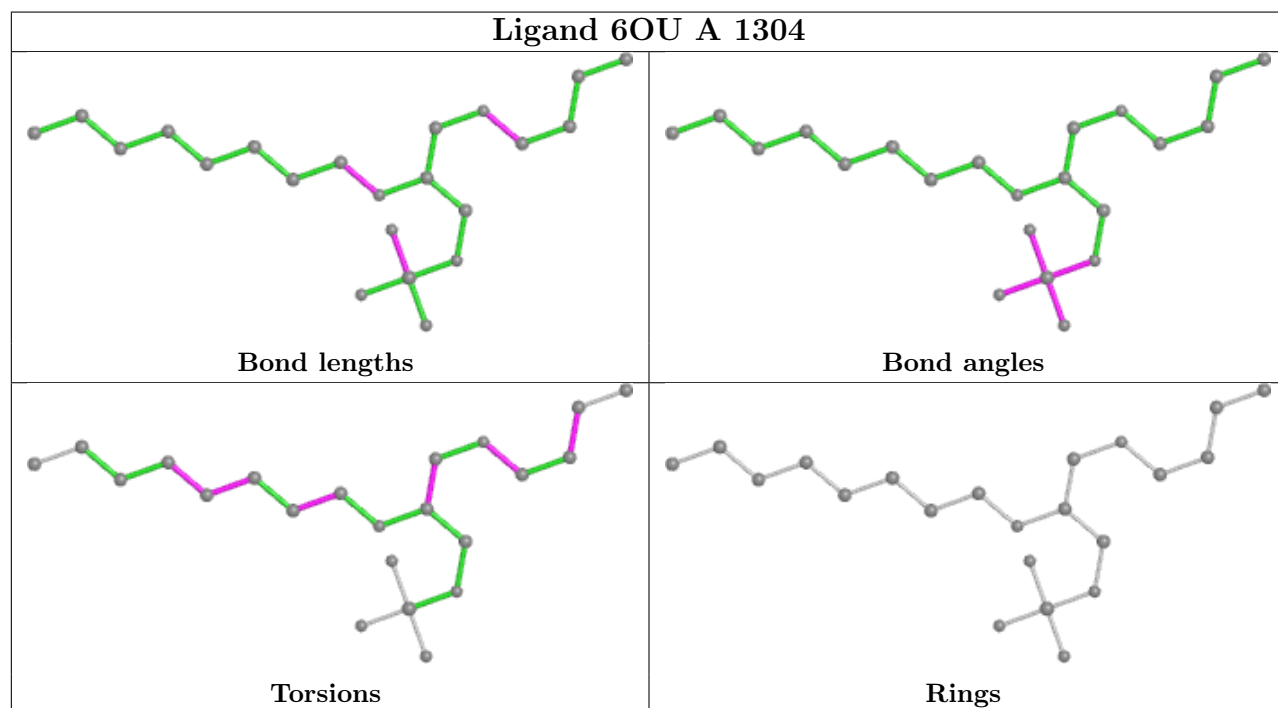
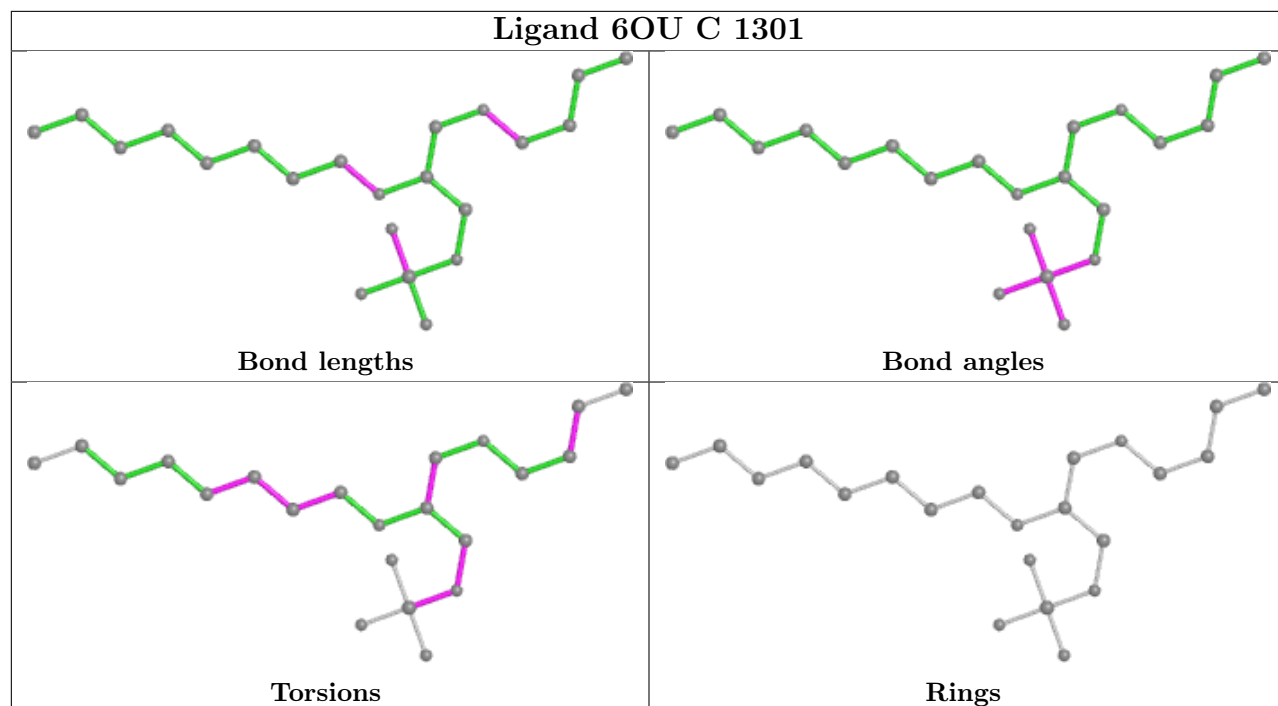
Mol	Chain	Res	Type	Atoms
4	B	1301	6OU	C21-O22-P23-O26
4	C	1301	6OU	C21-O22-P23-O24
4	C	1301	6OU	C21-O22-P23-O25

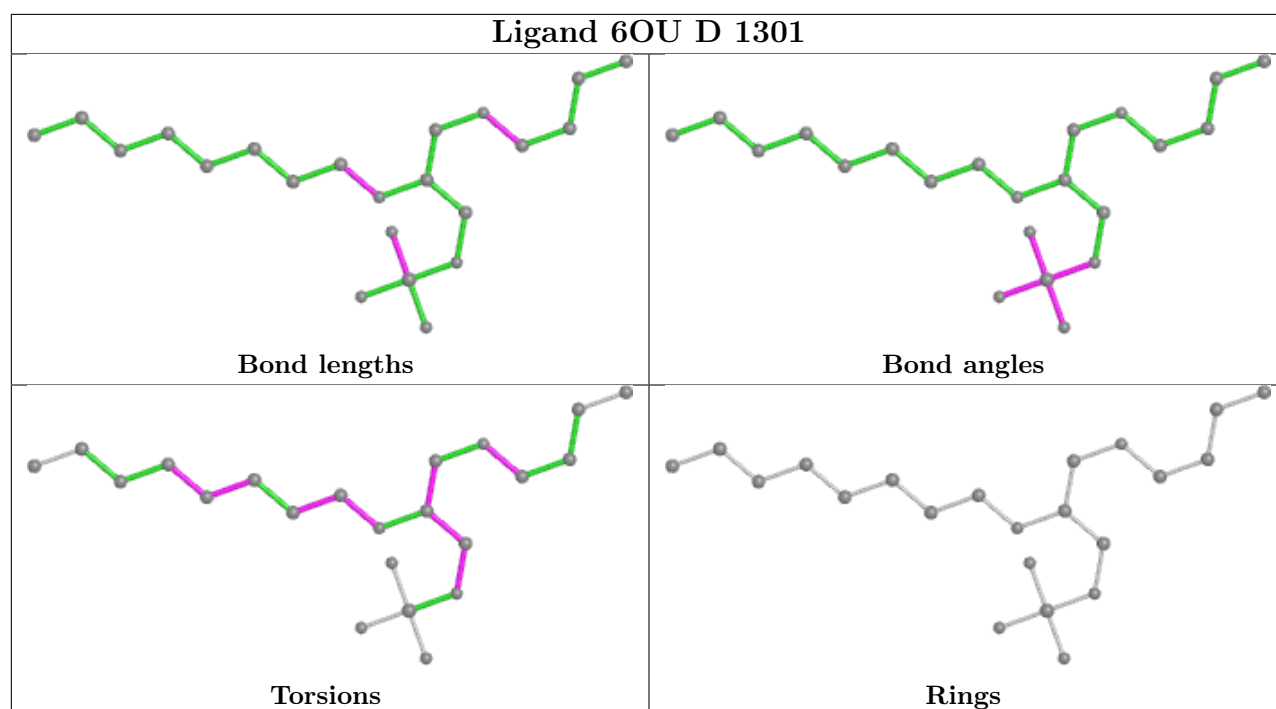
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

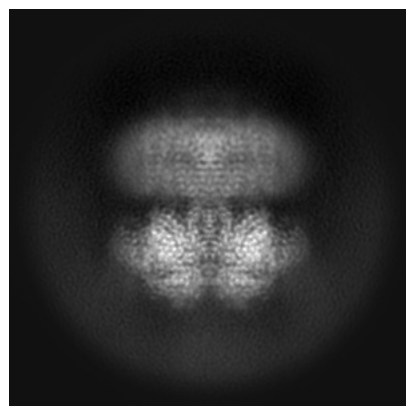
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34855. These allow visual inspection of the internal detail of the map and identification of artifacts.

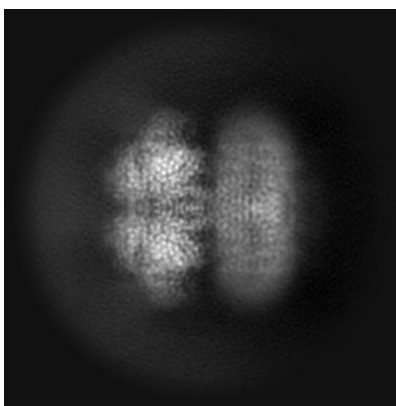
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

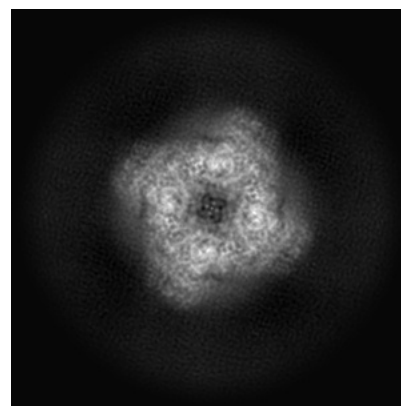
6.1.1 Primary map



X

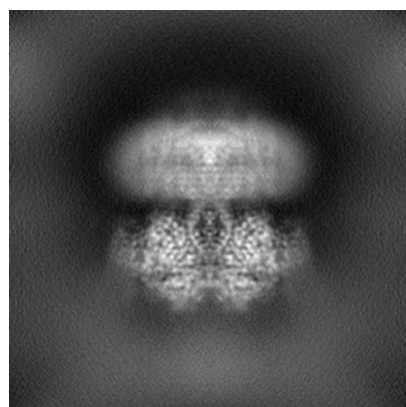


Y

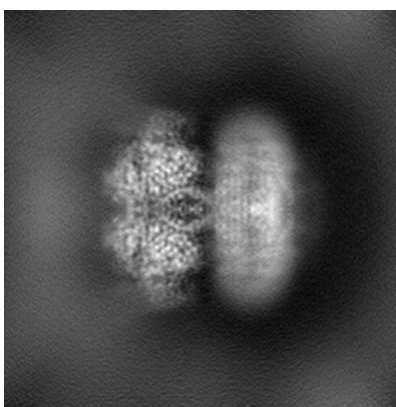


Z

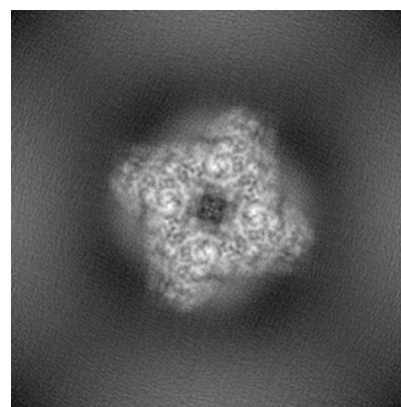
6.1.2 Raw map



X



Y

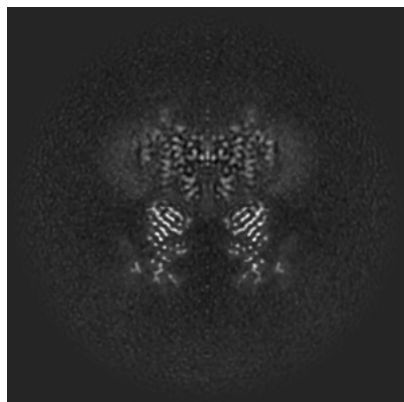


Z

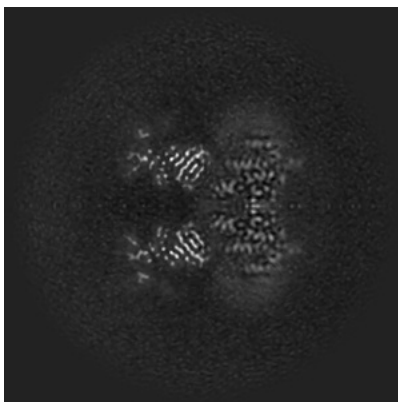
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

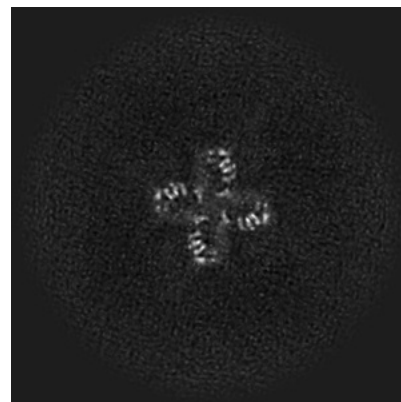
6.2.1 Primary map



X Index: 128

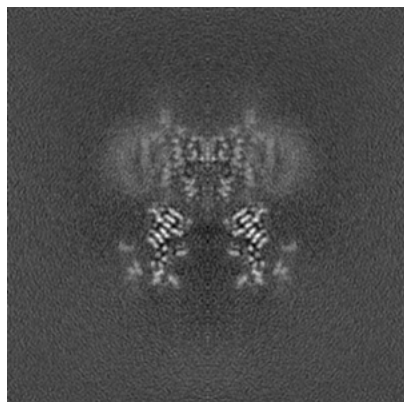


Y Index: 128

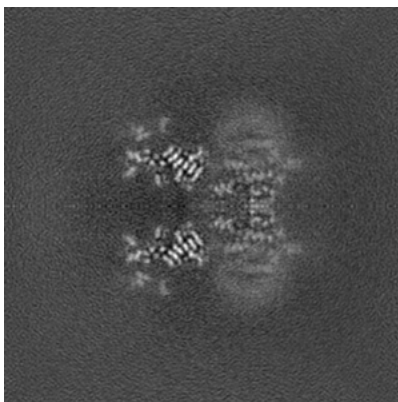


Z Index: 128

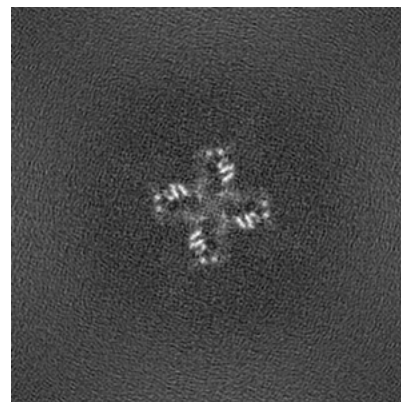
6.2.2 Raw map



X Index: 128



Y Index: 128

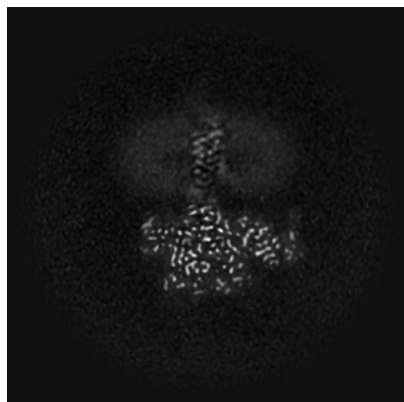


Z Index: 128

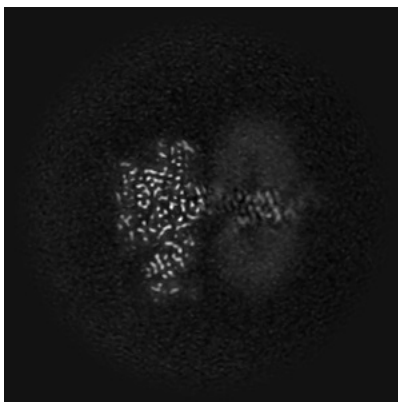
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

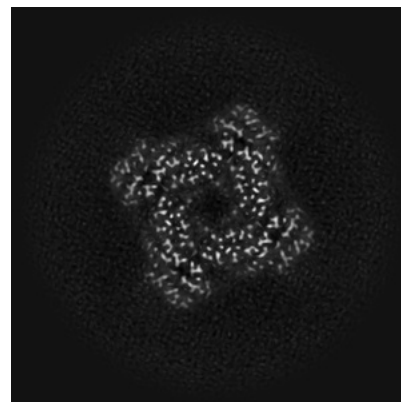
6.3.1 Primary map



X Index: 158

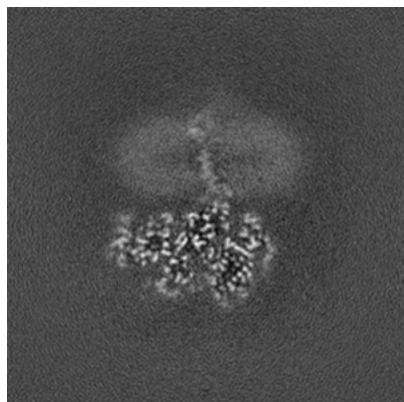


Y Index: 158

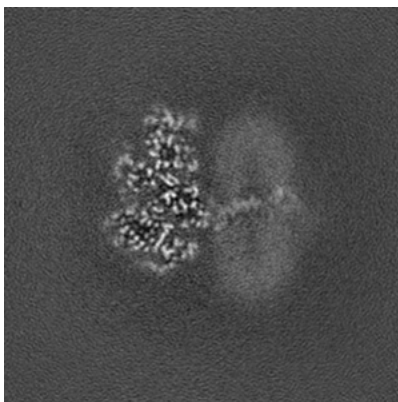


Z Index: 103

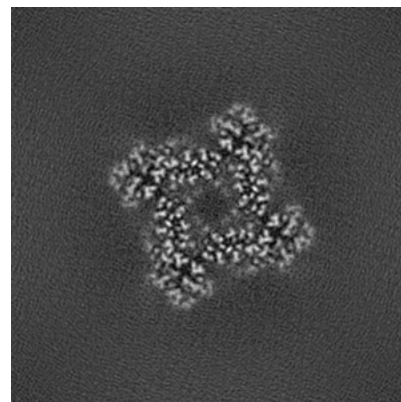
6.3.2 Raw map



X Index: 103



Y Index: 103

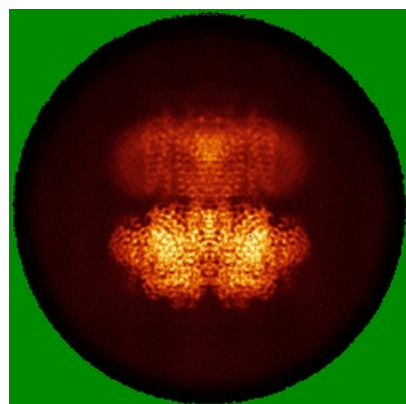


Z Index: 102

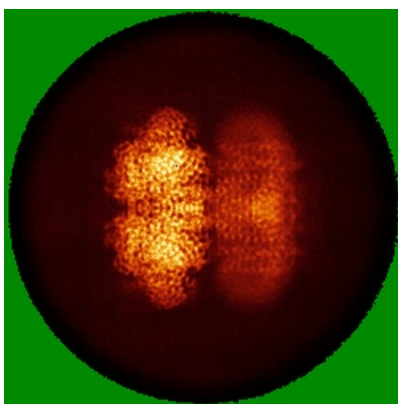
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

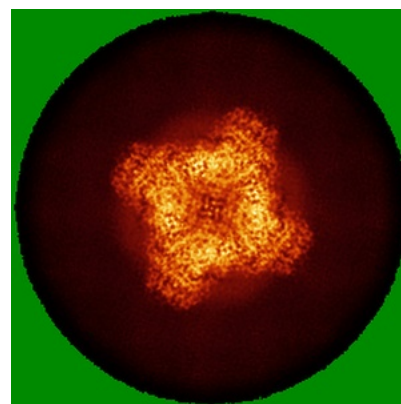
6.4.1 Primary map



X

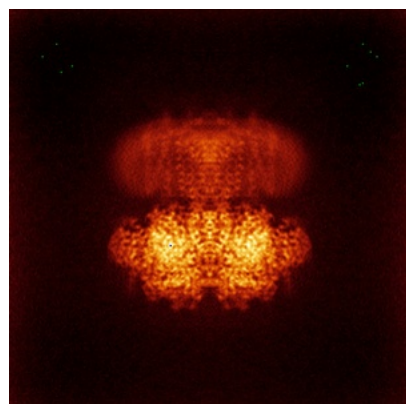


Y

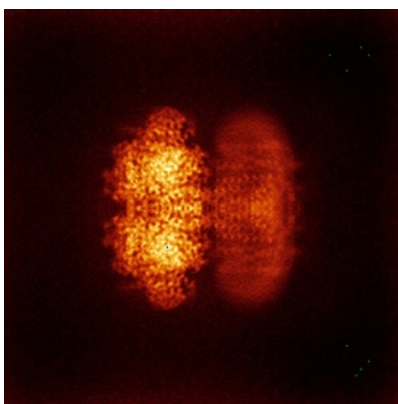


Z

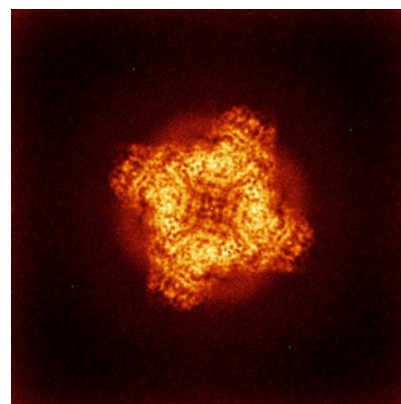
6.4.2 Raw map



X



Y

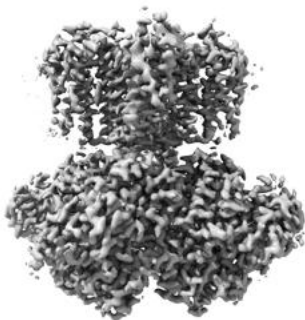


Z

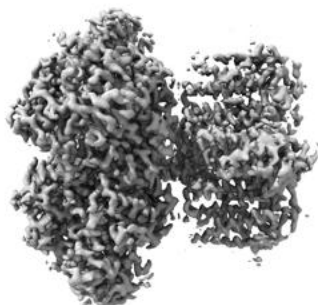
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

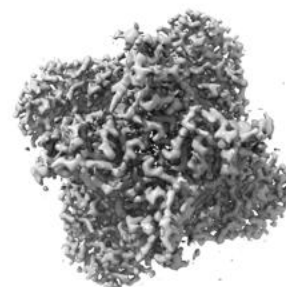
6.5.1 Primary map



X



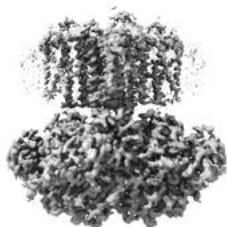
Y



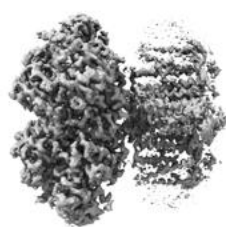
Z

The images above show the 3D surface view of the map at the recommended contour level 0.612. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

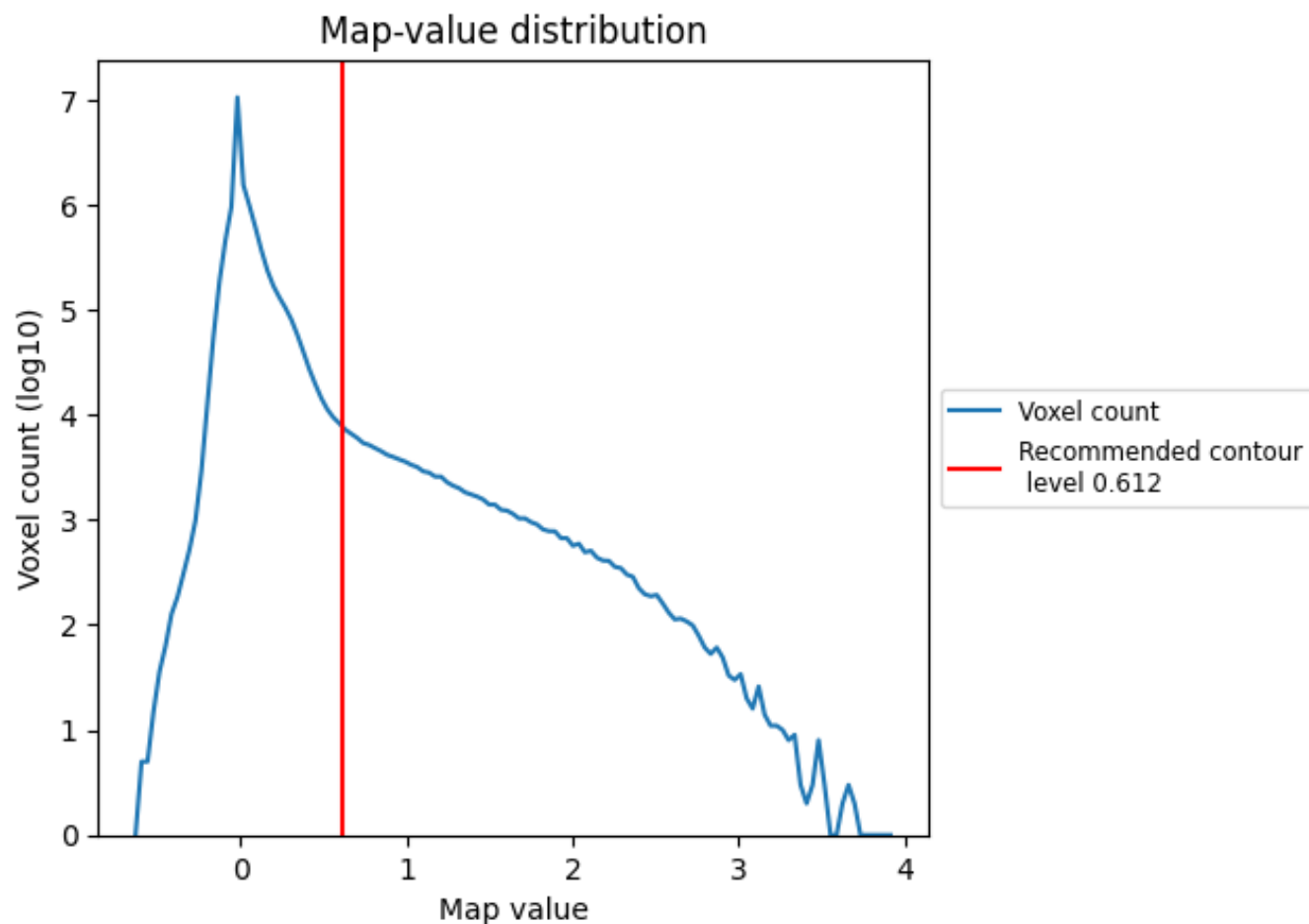
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

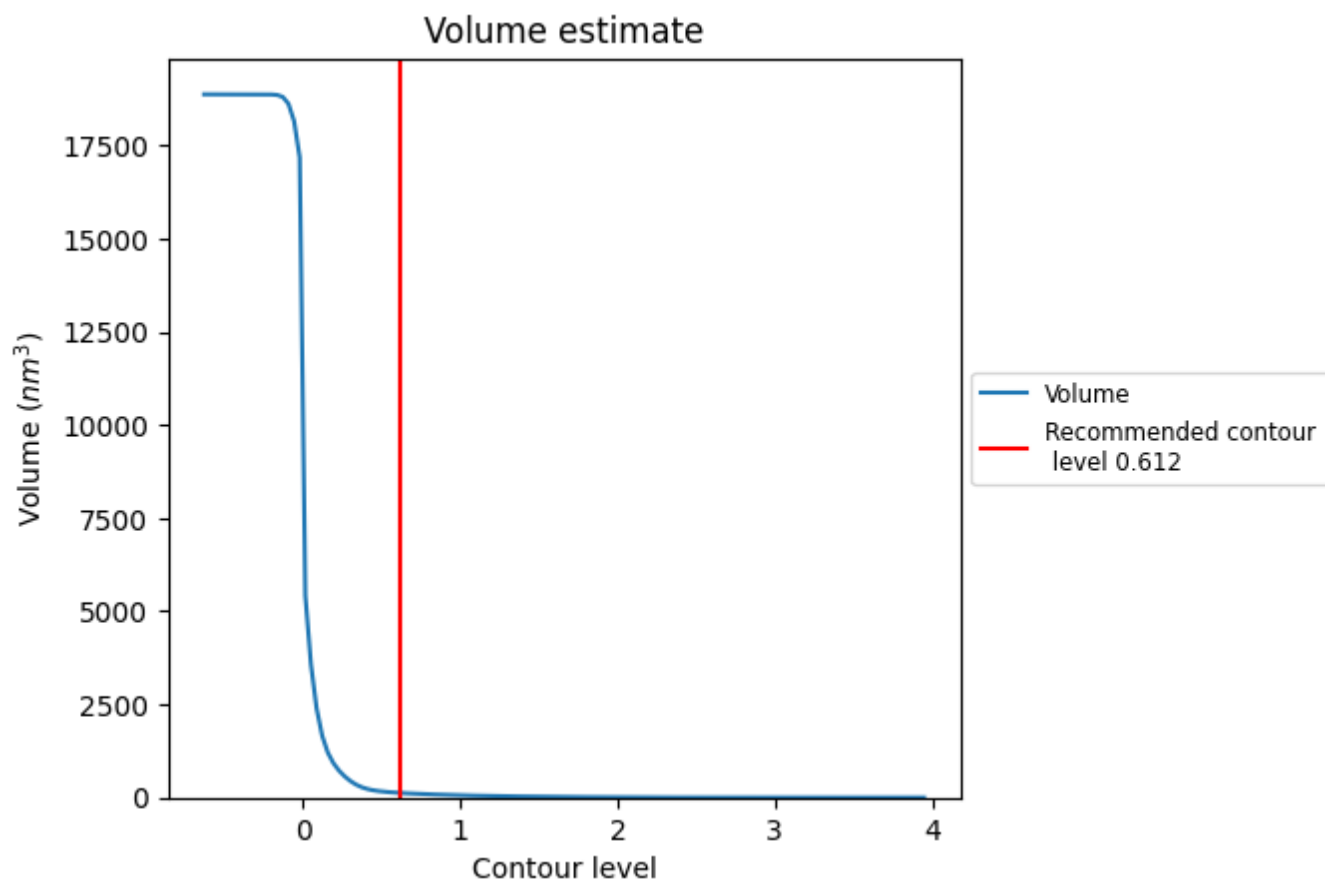
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

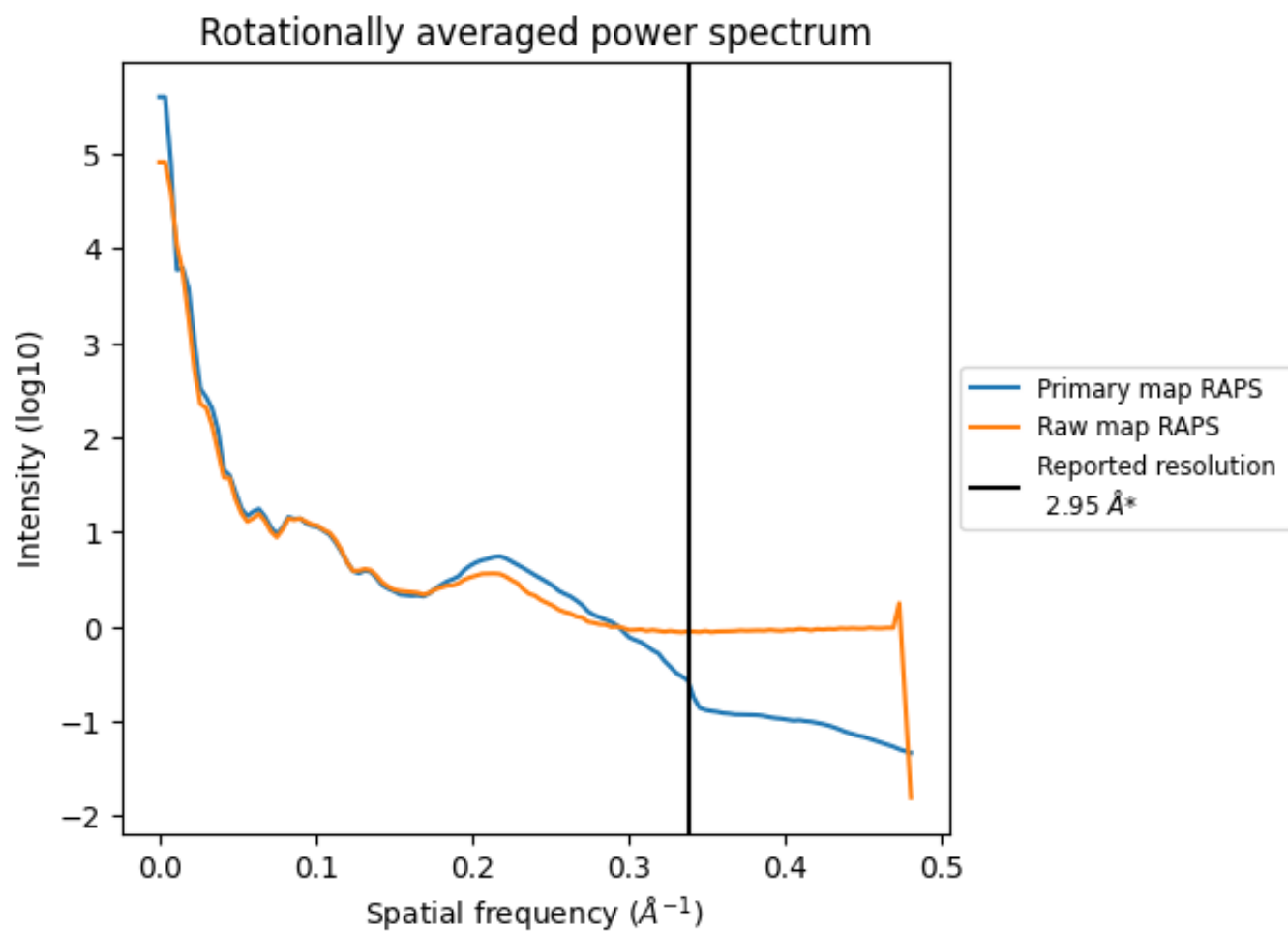
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 126 nm³; this corresponds to an approximate mass of 114 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

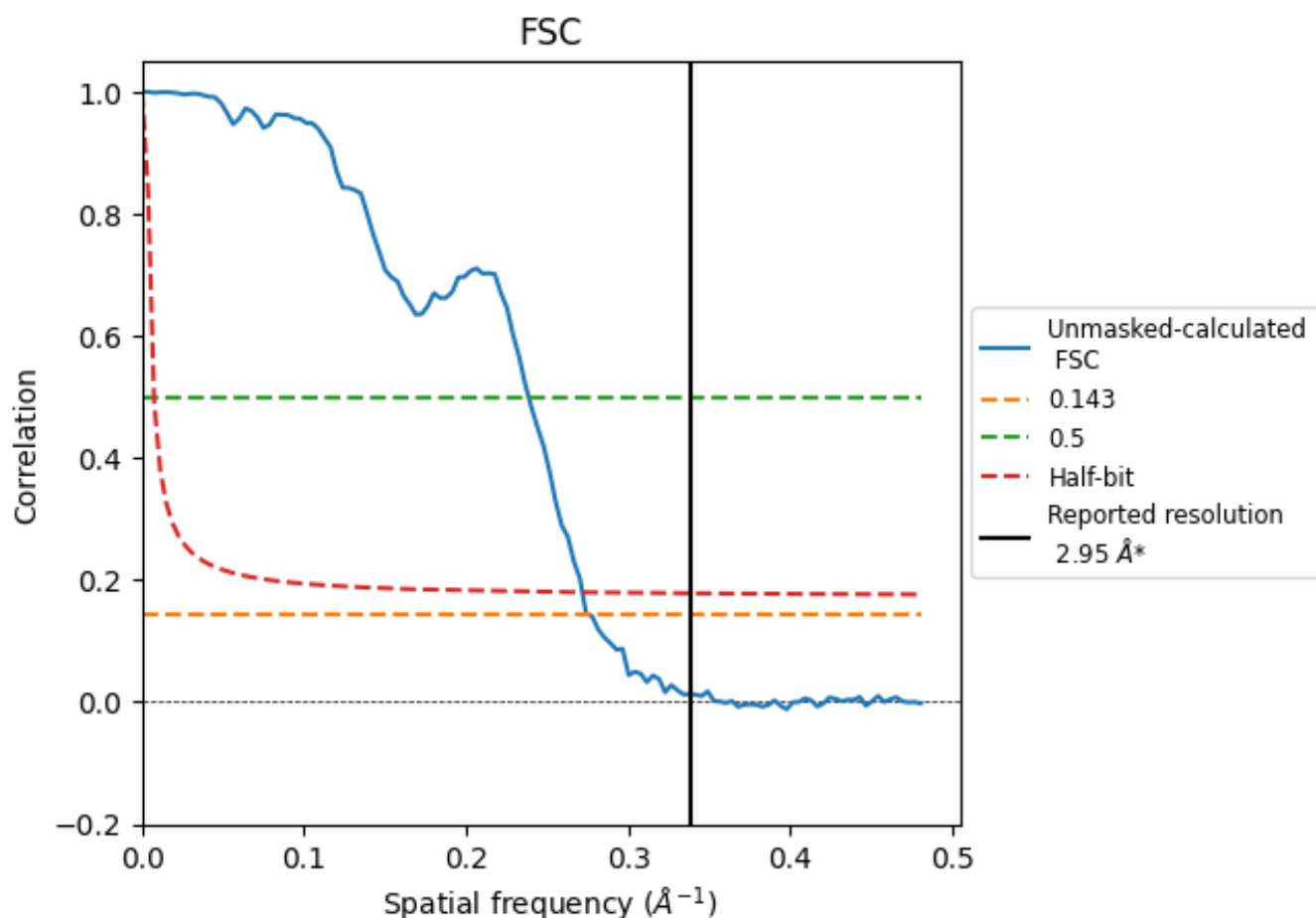


*Reported resolution corresponds to spatial frequency of 0.339 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.339 Å⁻¹

8.2 Resolution estimates [i](#)

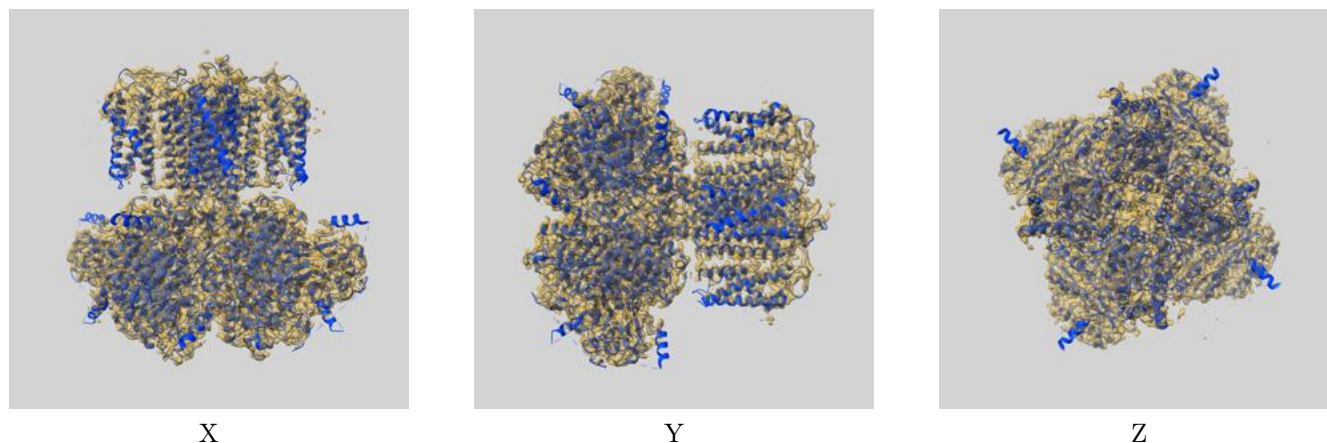
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.95	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.63	4.19	3.68

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.63 differs from the reported value 2.95 by more than 10 %

9 Map-model fit [i](#)

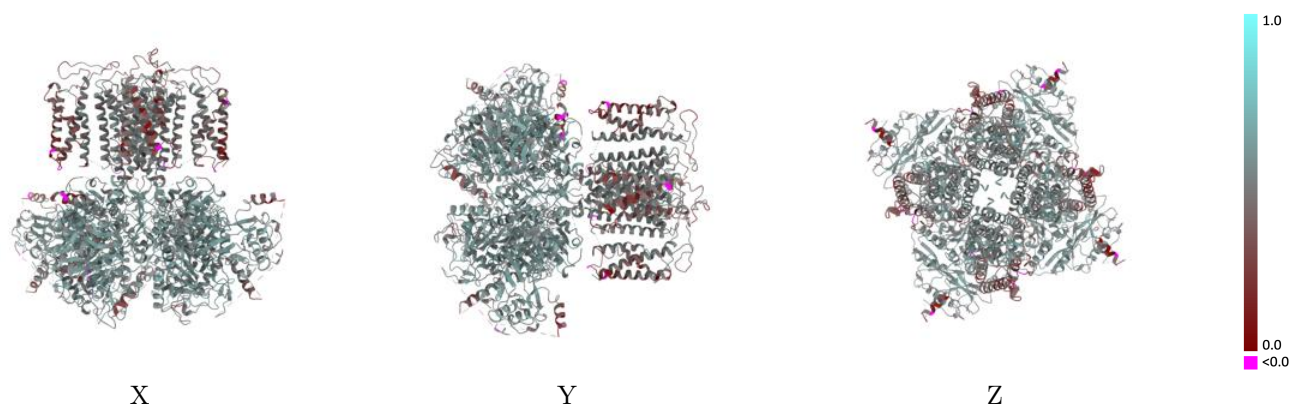
This section contains information regarding the fit between EMDB map EMD-34855 and PDB model 8HKM. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



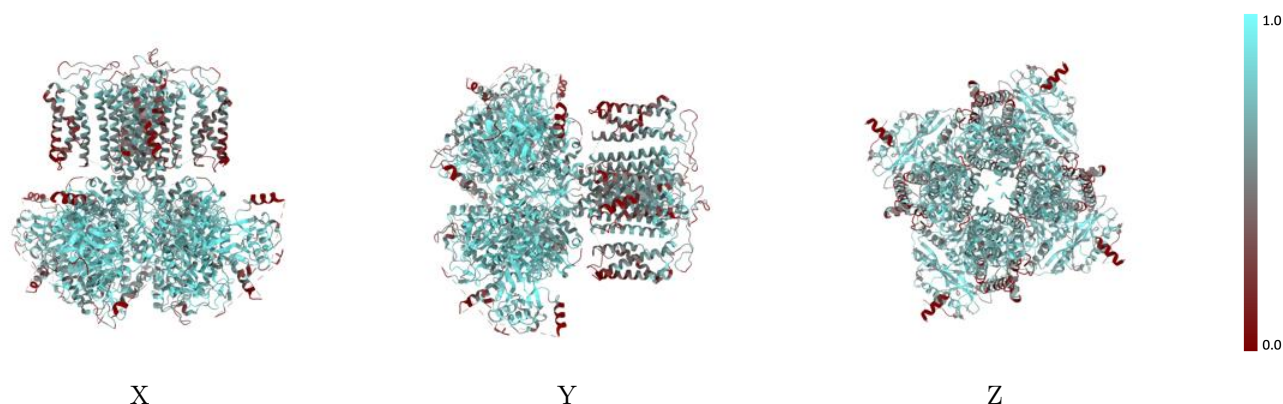
The images above show the 3D surface view of the map at the recommended contour level 0.612 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



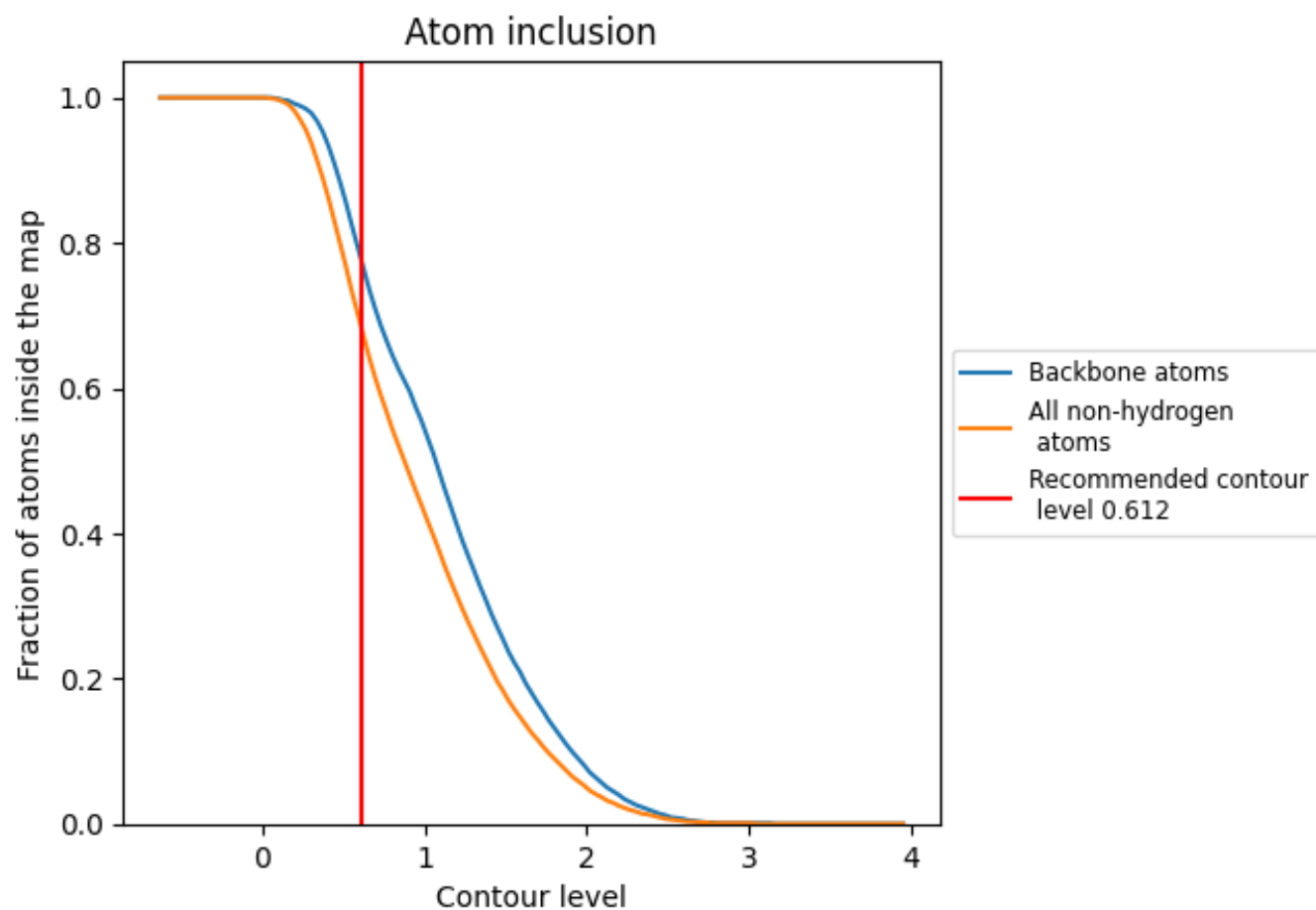
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.612).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.612) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6820	<div></div> 0.5120
A	<div></div> 0.6850	<div></div> 0.5140
B	<div></div> 0.6840	<div></div> 0.5110
C	<div></div> 0.6780	<div></div> 0.5100
D	<div></div> 0.6820	<div></div> 0.5120

